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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2007; month=12; day=29; hr=9; min=42; sec=8; ms=156;]

=====

Reviewer Comments:

<210> 9

<211> 1421

<212> DNA

<213> murine

<220>

<221> misc_feature

<222> (40)..(40)

<223> n = degenefacy in code

<400> 9

The above "n" response for sequence id# 9 is invalid, please explain
"n" location.

FYI, "n"s can only represent a single nucleotide.

Application No: 10559438 Version No: 2.0

Input Set:**Output Set:**

Started: 2007-12-03 19:59:20.899
Finished: 2007-12-03 19:59:25.633
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 734 ms
Total Warnings: 86
Total Errors: 0
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2007-12-03 19:59:20.899
Finished: 2007-12-03 19:59:25.633
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 734 ms
Total Warnings: 86
Total Errors: 0
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (21)
W 402	Undefined organism found in <213> in SEQ ID (22)
W 402	Undefined organism found in <213> in SEQ ID (23)
W 402	Undefined organism found in <213> in SEQ ID (24) This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (44)
W 213	Artificial or Unknown found in <213> in SEQ ID (85)

SEQUENCE LISTING

<110> McWhirter, John

<120> CELL SURFACE PROTEIN ASSOCIATED WITH HUMAN CHRONIC LYMPHOCYTIC
LEUKEMIA

<130> ALEX-P01-107

<140> 10559438

<141> 2007-12-03

<150> US 60/530,094

<151> 2003-12-15

<150> US 60/475,156

<151> 2003-06-02

<160> 86

<170> PatentIn version 3.2

<210> 1

<211> 183

<212> PRT

<213> human

<400> 1

Met	Gln	Ala	Pro	Arg	Ala	Ala	Leu	Val	Phe	Ala	Leu	Val	Ile	Ala	Leu
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Val	Pro	Val	Gly	Arg	Gly	Asn	Tyr	Glu	Glu	Leu	Glu	Asn	Ser	Gly	Asp
			20					25					30		

Thr	Thr	Val	Glu	Ser	Glu	Arg	Pro	Asn	Lys	Val	Thr	Ile	Pro	Ser	Thr
		35					40					45			

Phe	Ala	Ala	Val	Thr	Ile	Lys	Glu	Thr	Leu	Asn	Ala	Asn	Ile	Asn	Ser
50						55					60				

Thr	Asn	Phe	Ala	Pro	Asp	Glu	Asn	Gln	Leu	Glu	Phe	Ile	Leu	Met	Val
65					70				75					80	

Leu	Ile	Pro	Leu	Ile	Leu	Leu	Val	Leu	Leu	Leu	Leu	Ser	Val	Val	Phe
			85					90						95	

Leu	Ala	Thr	Tyr	Tyr	Lys	Arg	Lys	Arg	Thr	Lys	Gln	Glu	Pro	Ser	Ser
			100				105						110		

Gln Gly Ser Gln Ser Ala Leu Gln Thr Tyr Glu Leu Gly Ser Glu Asn
115 120 125

Val Lys Val Pro Ile Phe Glu Glu Asp Thr Pro Ser Val Met Glu Ile
130 135 140

Glu Met Glu Glu Leu Asp Lys Trp Met Asn Ser Met Asn Arg Asn Ala
145 150 155 160

Asp Phe Glu Cys Leu Pro Thr Leu Lys Glu Glu Lys Glu Ser Asn His
165 170 175

Asn Pro Ser Asp Ser Glu Ser
180

<210> 2
<211> 675
<212> DNA
<213> human

<400> 2
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tccccgcgca gccctagtct tcgccctggt gatcgcgctc gttcccgtcg gccggggtaa 120
ttatgaggaa ttagaaaact caggagatac aactgtggaa tctgaaagac caaataaagt 180
gactattcca agcacatttg ctgcagtgac catcaaagaa acattaaatg caaatataaa 240
ttctaccaac tttgctccgg atgaaaatca gttagagttt atactgatgg tgттаатccc 300
attgatttta ttggtcctct tacttttatac cgtgggtattc cttgcaacat actataaaag 360
aaaaagaact aacaagaacc ttctagccaa ggatctcaga gtgctttaca gacatatgaa 420
ctgggaagtg aaaacgtgaa agtccttatt tttgaggaag atacaccctc tgttatggaa 480
attgaaatgg aagagcttga taaatggatg aacagcatga atagaaatgc cgactttgaa 540
tgtttaccta ccttgaagga agagaaggaa tcaaatacaca acccaagtga cagtgaatcc 600
taaacctgaa tggcgctcat gttttccaag agaagcagcc cctgagggag tctgctgagg 660
ctgccaacag gatcc 675

<210> 3
<211> 181
<212> PRT
<213> murine

<400> 3

Met Thr Val Pro Cys Ala Ala Leu Val Leu Ala Leu Gly Leu Ala Phe
1 5 10 15

Gly Gln Ser Ser Gln Gly Asn Asp Glu Glu Ser Glu Tyr Ser Gly Gln
20 25 30

Ser Ile Thr Glu Glu Glu Asn Ser Glu Asp Glu Thr Thr Arg Ser Ala
35 40 45

Leu Ala Thr Val Thr Thr Glu Ala Leu Ala Glu Asn Val Asn Ser Thr
50 55 60

His Thr Asn Asp Thr Ser Asn Gln Val Glu Phe Ile Leu Met Val Ala
65 70 75 80

Ile Pro Leu Ala Ala Leu Leu Ile Leu Leu Phe Met Val Leu Ile Ala
85 90 95

Thr Tyr Phe Lys Ser Lys Arg Pro Lys Gln Glu Pro Ser Ser Gln Gly
100 105 110

Ser Gln Ser Ala Leu Gln Thr His Glu Leu Gly Gly Glu Thr Leu Lys
115 120 125

Val Pro Ile Phe Glu Glu Asp Thr Pro Ser Val Met Glu Ile Glu Met
130 135 140

Glu Glu Leu Asp Lys Trp Met Asn Ser Met Asn Arg Asn Ala Asp Tyr
145 150 155 160

Glu Cys Leu Pro Thr Leu Lys Glu Glu Lys Glu Pro Asn Pro Ser Pro
165 170 175

Ser Asp Asn Glu Ser
180

<210> 4
<211> 367
<212> PRT
<213> rat

<400> 4

Met Thr Arg Pro Pro Tyr Gln Glu Ala Pro Val Gly Asp Leu Gln Met
1 5 10 15

Gly Asp Arg Gln Glu Ser Ser Gly Asp Lys Asp Arg Asn Asp Glu Asp
20 25 30

Ser Glu Tyr Ser Gly His Ser Thr Thr Glu Glu Asp Thr Ala Glu Glu
35 40 45

Glu Thr Thr Arg Ala Leu Ala Thr Val Thr Thr Glu Ala Leu Ala Glu
50 55 60

Ser Ala Asn Ser Thr His Ile His Gly Thr Ser Asn Gln Val Glu Phe
65 70 75 80

Ile Leu Met Val Ala Val Pro Leu Ala Ala Leu Leu Ile Leu Leu Phe
85 90 95

Ala Ile Leu Ile Val Ile Tyr Phe Lys Ser Arg Arg Pro Lys Gln Glu
100 105 110

Pro Ser Ser Gln Gly Ser Gln Ser Ala Leu Gln Thr Leu Arg Leu Leu
115 120 125

Leu Ser Leu Glu Thr Lys Arg Pro Glu Pro Ser Val Ala Pro Ser Leu
130 135 140

Gly Pro Arg Pro Thr Ile Pro Leu Pro Thr Ala Gln Arg Gly Pro Cys
145 150 155 160

Gln Gln Ser Gly Cys Lys Ala Gly Thr Lys Gly Gly Arg Gln Asp Arg
165 170 175

Gly Glu Asn Glu Met Ala Gly Arg Lys Gly Thr Lys Trp Lys Pro Val
180 185 190

Gly Asn Gly Pro Gly Ala Glu Lys Met Arg Pro Gln Lys Ala Phe Cys
195 200 205

Ser Phe Asn Ala Asp Tyr Gly Ala Ser His Ser Val His Leu Glu His
210 215 220

Phe Gly Asn Gly Phe Leu Asn Phe Ser Ile Ile Cys Met Gln Val Gly

225

230

235

240

Phe Cys Pro Pro Pro Ser Leu Trp Gly Ala Gln Met Arg Val Glu Ile

245250255

Arg Ala His Ser Gly Thr Val Glu Pro Leu Ala Val Trp Glu Ile Gly

260265270

Gly Glu Val Ala Lys Gln Gly Lys Gly Thr Asp Asp Leu Gly Gly Glu

275280285

Thr Leu Lys Val Pro Ile Phe Glu Glu Asp Thr Pro Ser Val Met Glu

290295300

Ile Glu Met Glu Glu Leu Asp Lys Trp Met Asn Ser Met Asn Arg Asn

305310315320

Gly Thr Trp Lys Thr Lys Ala Phe Ala Cys Leu Cys Gly Asn Ala Gly

325330335

Leu Asp Gly Cys Leu Cys Phe Ile Ser Asn Ser Glu Asn Leu Lys Leu

340345350

Cys Phe Ile Trp His Ser Thr Cys Ala Leu Leu Lys Asp Pro Val

355360365

<210> 5

<211> 703

<212> DNA

<213> artificial sequence

<220>

<223> FLJ32028 with an HA epitope tag

<400> 5

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60

tccccgcgca gccctagttc tcgccctggg gatcgcgcctc gttcccgtcg gccgggggtaa

120

ttatccatat gatgttccag attatgctta tgaggaatta gaaaactcag gagatacaac

180

tgtggaatct gaaagaccaa ataaagtgac tattccaagc acatttgctg cagtgaccat

240

caaagaaaca ttaaatagcaa atataaattc taccaacttt gctccggatg aaaatcagtt

300

agagtttata ctgatgggtg taatcccatt gattttattg gtccctcttac ttttatccgt

360

ggtattcctt gcaacatact ataaaagaaa aagaactaaa caagaacctt ctagccaagg

420

atctcagagt gctttacaga catatgaact gggaagtgaa aacgtgaaag tccctatttt 480
tgaggaagat acaccctctg ttatggaaat tgaaatggaa gagcttgata aatggatgaa 540
cagcatgaat agaaatgccg actttgaatg tttacctacc ttgaaggaag agaaggaatc 600
aatcacaac ccaagtgaca gtgaatccta aacctgaatg gcgctcatgt tttccaagag 660
aagcagcccc tgagggagtc tgctgaggct gccaacagga tcc 703

<210> 6
<211> 192
<212> PRT
<213> artificial sequence

<220>
<223> FLJ32028 with HA epitope tag

<400> 6

Met Gln Ala Pro Arg Ala Ala Leu Val Phe Ala Leu Val Ile Ala Leu
1 5 10 15

Val Pro Val Gly Arg Gly Asn Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
20 25 30

Tyr Glu Glu Leu Glu Asn Ser Gly Asp Thr Thr Val Glu Ser Glu Arg
35 40 45

Pro Asn Lys Val Thr Ile Pro Ser Thr Phe Ala Ala Val Thr Ile Lys
50 55 60

Glu Thr Leu Asn Ala Asn Ile Asn Ser Thr Asn Phe Ala Pro Asp Glu
65 70 75 80

Asn Gln Leu Glu Phe Ile Leu Met Val Leu Ile Pro Leu Ile Leu Leu
85 90 95

Val Leu Leu Leu Leu Ser Val Val Phe Leu Ala Thr Tyr Tyr Lys Arg
100 105 110

Lys Arg Thr Lys Gln Glu Pro Ser Ser Gln Gly Ser Gln Ser Ala Leu
115 120 125

Gln Thr Tyr Glu Leu Gly Ser Glu Asn Val Lys Val Pro Ile Phe Glu
130 135 140

Glu Asp Thr Pro Ser Val Met Glu Ile Glu Met Glu Glu Leu Asp Lys
145 150 155 160

Trp Met Asn Ser Met Asn Arg Asn Ala Asp Phe Glu Cys Leu Pro Thr
165 170 175

Leu Lys Glu Glu Lys Glu Ser Asn His Asn Pro Ser Asp Ser Glu Ser
180 185 190

<210> 7
<211> 637
<212> DNA
<213> artificial sequence

<220>
<223> FLJ32028 with HA epitope tag

<400> 7
aagcttagcc cggcgcagca tcttgagcgc gcctctgccg aggcgagcgg acatgcaggc 60

tccccgcgca gccctagtct tcgccctggg gatcgcgctc gttcccgctc gccggggtaa 120

ttatgaggaa ttagaaaact caggagatac aactgtggaa tctgaaagac caataaagt 180

gactattcca agcacatttg ctgcagtgac catcaaagaa acattaaatg caaatataaa 240

ttctaccaac tttgctccgg atgaaaatca gttagagttt atactgatgg tgttaatccc 300

attgatttta ttggtcctct tacttttata cgtgggtattc cttgcaacat actataaaag 360

aaaaagaact aaacaagaac cttctagcca aggatctcag agtgctttac agacatatga 420

actgggaagt gaaaacgtga aagtccttat ttttgaggaa gatacacct ctgttatgga 480

aattgaaatg gaagagcttg ataaatggat gaacagcatg aatagaaatg ccgactttga 540

atgtttacct accttgaagg aagagaagga atcaaatac aaccaagtg acagtgaatc 600

ctatccatat gatgttccag attatgctta aggatcc 637

<210> 8
<211> 192
<212> PRT
<213> artificial sequence

<220>
<223> FLJ32028 with HA epitope tag

<400> 8

Met Gln Ala Pro Arg Ala Ala Leu Val Phe Ala Leu Val Ile Ala Leu
1 5 10 15

Val Pro Val Gly Arg Gly Asn Tyr Glu Glu Leu Glu Asn Ser Gly Asp
20 25 30

Thr Thr Val Glu Ser Glu Arg Pro Asn Lys Val Thr Ile Pro Ser Thr
35 40 45

Phe Ala Ala Val Thr Ile Lys Glu Thr Leu Asn Ala Asn Ile Asn Ser
50 55 60

Thr Asn Phe Ala Pro Asp Glu Asn Gln Leu Glu Phe Ile Leu Met Val
65 70 75 80

Leu Ile Pro Leu Ile Leu Leu Val Leu Leu Leu Leu Ser Val Val Phe
85 90 95

Leu Ala Thr Tyr Tyr Lys Arg Lys Arg Thr Lys Gln Glu Pro Ser Ser
100 105 110

Gln Gly Ser Gln Ser Ala Leu Gln Thr Tyr Glu Leu Gly Ser Glu Asn
115 120 125

Val Lys Val Pro Ile Phe Glu Glu Asp Thr Pro Ser Val Met Glu Ile
130 135 140

Glu Met Glu Glu Leu Asp Lys Trp Met Asn Ser Met Asn Arg Asn Ala
145 150 155 160

Asp Phe Glu Cys Leu Pro Thr Leu Lys Glu Glu Lys Glu Ser Asn His
165 170 175

Asn Pro Ser Asp Ser Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
180 185 190

<210> 9
<211> 1421
<212> DNA
<213> murine

<220>
<221> misc_feature
<222> (40)..(40)
<223> n = degenefacy in code

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acctgcagaa accaggccag tctccaaagc tcctgatcta caaagtttcc aaccgatttt 180

ctgggggtccc agacagggtc agtggcagtg gatcaggggac agatttcaca ctcaagatca 240

gcagagtgga ggctgaggat ctgggagttt attactgctt tcaagggtca catgttccgc 300

tcacgttcgg tgctgggacc aagctggagc tgaaacgggc tgatgctgca ccaactgtat 360

ccatcttccc accatccagt gagcagttaa catccggagg tgctcagtc gtgtgcttct 420

tgaacaactt ctaccccaaa gacatcaatg tcaagtggaa gattgatggc agtgaacgac 480

aaaatggcgt cctgaacagt tggactgatc aggacagcaa agacagcacc tacagcatga 540

gcagcaccct cacgttgacc aaggacgagt atgaacgaca taacagctat acctgtgagg 600

ccactcacia gacatcaact tcacccattg tcaagagctt caacaggaat gagtgttaag 660

cggccgcact agatataatt aaggagataa atatgaaata tctgctgccg accgcggcgg 720

cgggcctgct gctgctggcg gcgcagccgg cgatggcgct cgaggtgaag ctggtggagt 780

ctggggggagg cttagtgaag cctggagggt ccctgaaact ctctgtgca gcctctggat 840

tcactttcag tgactatgcc atgtcttggg ttcgccagac tccagagaag aggctggagt 900

gggtcgcac aattagtagt ggtggtacca cctattatct agacagtgtg aagggccgat 960

tcaccatctc cagagataat gccaggaaca tcctgtacct gcaaatgagc agtctgaggt 1020

ctgaggacac ggccatgtat tattgtgtaa gaagtgagac gaactactgg ggccaaggca 1080

ccactctcac agtctcctca gccaaaacga ccccccatc tgtctatcca ctggcccctg 1140

gatctgctgc ccaaactaac tccatgataa ccctaggctg cctggtcaag gactacttcc 1200

ccgaaccggt gacggtgtcg tggaactcag gcgctctgac cagcggcgtg cacaccttcc 1260

cggtgtcct acagtctca ggactctact ccctcagcag cgtggtgacc gtgccatcca 1320

gcagcttggg caccagacc tacatctgca acgtgaatca caagcccagc aacaccaagg 1380

tggaacaagaa agttgagccc aaatcttgtg aaaaaactag t 1421

<210> 10
<211> 474
<212> PRT
<213> murine

<220>

<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (220)..(220)
<223> Xaa = any amino acid

<400> 10

Tyr Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Xaa Phe Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
115 120 125

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
130 135 140

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
145 150 155 160

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
180 185 190

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
195 200 205

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Xaa Ala Ala Ala Leu
210 215 220

Asp Ile Ile Lys Glu Ile Asn Met Lys Tyr Leu Leu Pro Thr Ala Ala
225 230 235 240

Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Leu Glu Val
245 250 255

Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu
260 265 270

Lys Leu Ser Cys